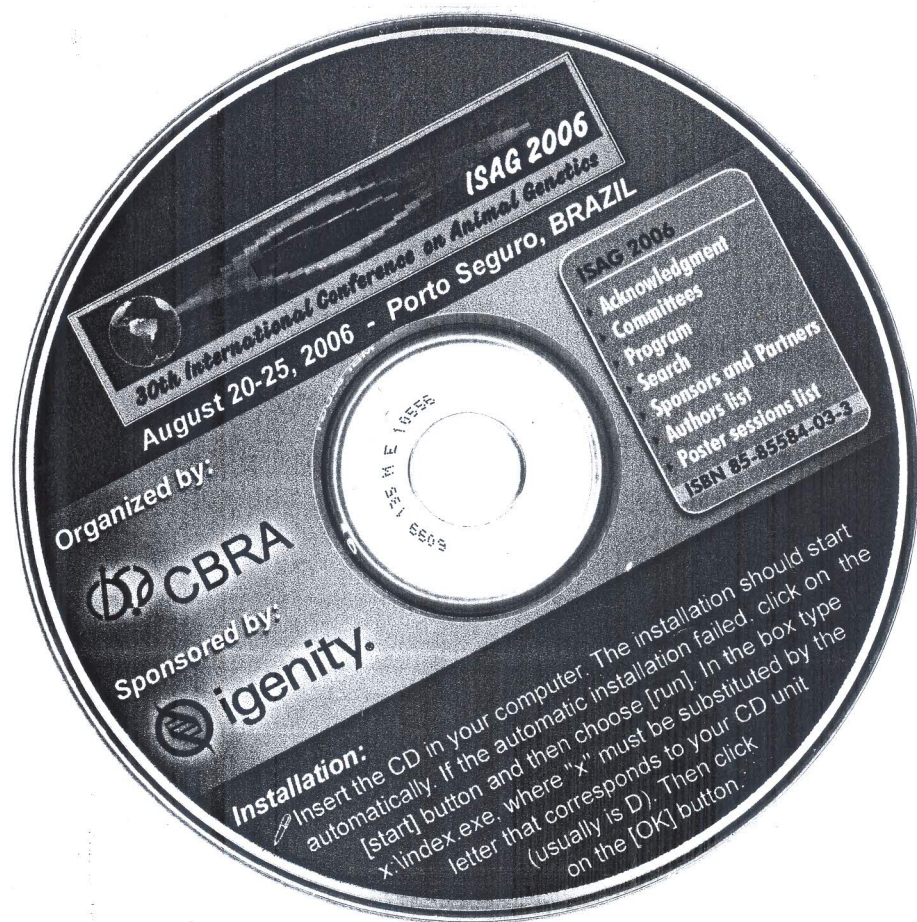


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Section A: Polymorphism and Biodiversity

Genetic variation at 23 STRs loci in five Brazilian populations of Santa Inês hair sheep breed

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Santa Inês is a naturalized sheep breed, known to be highly adapted to the most diverse and harsh Brazilian ecosystems. As part of a concerted effort to increase its production potential through selective breeding it became imperative to adopt DNA marker typing to verify animal parentage and origin. In this study, a database of allele frequencies of Santa Inês hair sheeps at 23 STRs loci is described. The loci genotyped were INRA23, OARFCB304, MAF214, INRA63, OARHH35, INRA35, OMHC1, ILSTS87, ILSTS05, ILSTS11, MAF65, BM827, OARFCB20, OARCP20, OARAE129, INRA172, HUI616, SRCRS05, BM6526, OARCP49, OARFCB11, D5S2 and SPSP113, 13 of which have been recommended as part of ISAG comparison tests marker panel for sheep. Data were collected from a total of 285 animals from five populations distributed along the Central-Western and North-Eastern states of Brazil. Overall, the set of microsatellites typed exhibited an average of 10 alleles, PIC value of 0.712 and average expected heterozygosity of 0.745. The cumulative probabilities of paternity exclusion, with and without one parent already known (PE1 and PE2 respectively) were 0.999999 and 0.999989. Among all 23 loci, 11 did not depart from Hardy-Weinberg Equilibrium expectations ($P \leq 0.001$) and three of the five populations studied displayed significant heterozygote deficit ($P \leq 0.001$). The database reported in this work can be directly applied for verifying parentage in sheep breed registers and analyses of genetic diversity of herds.